

FIGURE 1 (SHEET 1)

1 TGAAGCTCAGCTGATGCAGCCCGTTGGAGTGACGCTCATTTGCCGGAGACGCGAGTC 60
 61 GCCCGTCAGCCCTAGTGAATGCGCCCTGCATCCCGATTGTCTTCTCCCAAGGCTTAC 120
 121 ATGATTACCTGAAGTTTAATAGTAAGACCATGAATTATGGCATTTCTTAATGAAGCGT 180
 181 TCAAGAAAGTGAGAAATGTCATAGAAAATAATGATTTTAAAGTATGCTATTAATCTG 240
 241 ACTGTAGATATATATATTACCTCTTAGTAATGCAAGAAGTGTGTTGGAGACAGAGA 300
 T V D I Y I Y L L S N A R S V C G K Q R
 301 AGCAAGCACTGTATTCTTGTCTCACCCTAAGCATTACTGGAGATAAGCCACATCAGT 360
 S K Q L Y F L F S P K H Y W R I S H I S
 361 CTACAAGAGGTTTCAATACAACATAATAAGATGTAATGACCAAAAGTGAAGCACAT 420
 L Q R G F H T N I I R C K W T K S E A H
 421 TCTTGACGTAAGCACTGTACTCTCCAAGCAACCATGGTTTACATATTGGGATTTGAAA 480
 S C S K H C Y S P S N H G L H I G I L K
 481 CTTAGCACTTCTGCTCCCAAGGACTTACAAAGTGAACATTTGTATGTCCCGATTAA 540
 L S T S A P K G L T K V N I C M S R I K
 541 AGTACTTTGAACCTGTGTTCAAGGCTGTTTGGCAATCAAAATGAATGATTTCCAGT 600
 S T L N S V S K A V F G N Q N E M I S R
 601 TTAGCTCAATTTAAGCCAGTTCCCAATTTTAAAGAAAGTATCGGATAGTGCGTTA 660
 L A Q F K P S S Q I L R K V S D S G W L
 661 AAACAGAAAACATCAACACAGCCATCAATCTCTGA AAAAATATAGTGAACAATCAGCA 720
 K Q K N I K Q A I K S L K K Y S D K S A
 721 GAAAAGAGTCCTTTCCAGAGAGAAAAGTCACTTATAGACAAAGAGAAGATATAGT 780
 E K S P F P E E K S H I I D K E E D I G
 781 AAACGAGCTTTTTCATTACACAAGTTCTATAACCAAAAATTTGGAGACTCATTTCTAC 840
 K R S L F H Y T S S I T T K F G D S F Y
 841 TTTTATCAATCATATTAATTATTTCAACGTAAGGAAAAATGTCTCAACAAAAG 900
 F L S N H I N S Y F K R K E K M S Q Q K
 901 GAAAATGACATTTCCGGAGCAAAATCAGAACTTGAAGATAAAAAGTAGAAGAGGGA 960
 E N E H F R D K S E L E D K K V E E G K
 961 TTAAGATCTCCAGATCCGTCATCTGCTTATAAGCCAGGCTCAGAATCTGTACATACG 1020
 L R S P D P G I L A Y K P G S E S V H T
 1021 GTGACAAAGCTACAAAGTCCTTCTGCGATACCTGATGTCTTCAAGTTTCAACTAAACA 1080

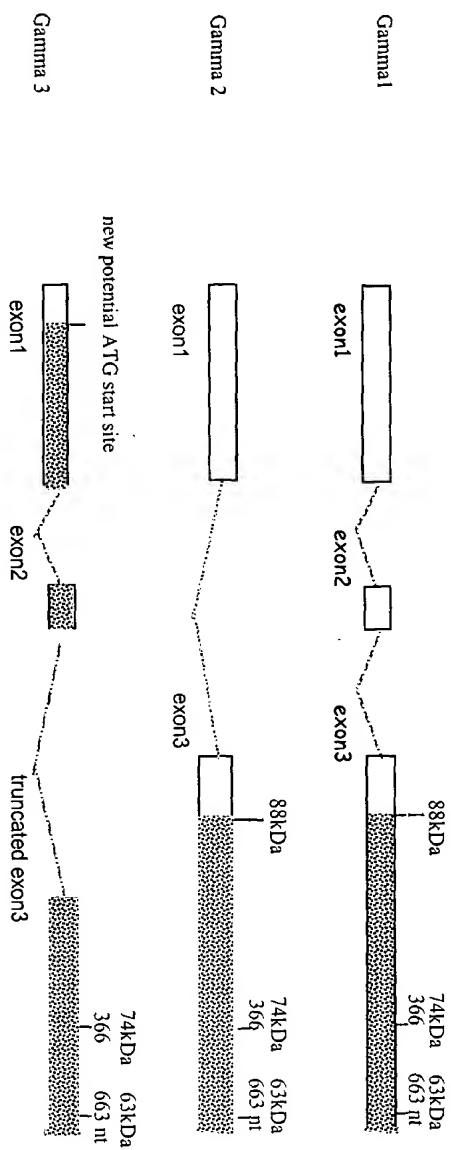
V	D	K	P	T	S	P	S	A	I	P	D	V	L	Q	V	S	T	K	Q	
1081	AGTATTGCTAACTTTCTTCTTCGTCCCGGAAGGTGTACAAGCTTTAGTAGTGTTAT	1140																		
	S	I	A	N	F	L	S	R	P	T	E	G	V	Q	A	L	V	G	Y	
1141	ATTGGTGACCTGTCCCCAATAATTAAAGTATGATTCAAGAGTCAGTCAGAAGAACAGGAA	1200																		
	I	G	G	L	V	P	K	L	K	Y	D	S	K	S	Q	S	E	E	Q	E
1201	GAGCCTGTAAAACTGATCAGGCTGTGCAGCAAAGACAGAAATGCAGAGGAGAAAAACCGT	1260																		
	E	P	A	K	T	D	Q	A	V	S	K	D	R	N	A	E	E	K	K	R
1261	TTATCTCTTCAGCGAAGAAAAGATTATTCGCAAGGTTAGTATTGATAACAGGACC CGGCA	1320																		
	L	S	L	Q	R	E	K	I	I	A	R	V	S	I	D	N	R	T	R	A
1321	TTAGTTCAGGCATTAGAAGAACAACACTGACCCAAAGCTCTGCATTACTAGGGTTGAAGAA	1380																		
	L	V	Q	A	L	R	R	T	T	D	P	K	L	C	I	T	R	V	E	E
1381	CTGACTTTTCATCTTCTAGAAATTTCCGTGAAGGAAAAGAGTGGCTGTCAAGGAAAGAATT	1440																		
	L	T	F	H	L	L	E	F	P	E	G	K	G	V	A	V	K	E	R	I
1441	ATTCCATATTATTACGACTGAGACAAATTAAAGATGAAACTCTTCAGGCTGCAGTTAGA	1500																		
	I	P	Y	L	L	R	L	R	Q	I	K	D	E	T	L	Q	A	A	V	R
1501	GAAATTTGGCCCTAATTGCCATGTGTGATCCAGTGAAAGGAGAGGAATCCGAATTCTC	1560																		
	E	I	L	A	L	I	G	Y	V	D	P	V	K	G	R	G	I	R	I	L
1561	TCAATTGATGGTGAGGAACAAGGGCGGTGCTCTCCAGACCCCTACGAAAATTAGTT	1620																		
	S	I	D	G	G	G	T	R	G	V	V	A	L	Q	T	L	R	K	L	V
1621	GAACTTACTCAGAAGCCAGTTTCATCAGCTCTTTGATTACATTTGTGTGTAAGCACAGGT	1680																		
	E	L	T	Q	K	P	V	H	Q	L	F	D	Y	I	C	G	V	S	T	G
1681	GCCATATTAGCTTTCATGTTGGGTTGTTTCATATGCCCCTTGATGAATGTGAGGAAC TT	1740																		
	A	I	L	A	F	M	L	G	L	F	H	M	P	L	D	E	C	E	E	L
1741	TATCGAAAATTAGATCAGATGATTTTTCACAAAATGTCA TTGTTGGAACAGTAAAAATG	1800																		
	Y	R	K	L	G	S	D	V	F	S	Q	N	V	I	V	G	T	V	K	M
1801	AGTTGAGCCATGCATTTTATGACAGTCACAACATGGGAAAAACATTTCTTAAGATAGATG	1860																		
	S	W	S	H	A	F	Y	D	S	Q	T	W	E	N	I	L	K	D	R	M
1861	GGATCTGCACATGATGATTGAACACAGCAAGAAACCCACATGTCTTAAGTAGCTGCTGTA	1920																		
	G	S	A	L	M	I	E	T	A	R	N	P	T	C	P	K	V	A	A	V
1921	AGTACCATTAGTAATAGAGGAGTAACACCCAAGCTTTTGTGTTCAGAAACTATGTCAT	1980																		
	S	T	I	V	N	R	G	I	T	P	K	A	F	V	F	R	N	Y	G	H
1981	TTTCCTGGAATCAACTCTCATTTATTTGGGAGGCGTGTCAGTATAAATGTGGCAGGCCATT	2040																		
	F	P	G	I	N	S	H	Y	L	G	G	C	Q	Y	K	M	W	Q	A	I

FIGURE 1 (SHEET 3)

2041 AGAGCCCTCATCTGCTGCTCCAGGCTACTTGCAGAAATATGCATTGGGAAATGATCTTCAT 2100
R A S S A A P G Y F A E Y A L G N D L H
2101 CAAGATGAGGTTTGCTTCTGAATAACCTTCGGCATTAGCTATGATGAGTSTAATGT 2160
Q D G G L L L N N P S A L A M H E C K C
2161 CTTGGCCAGATGTGCCGTTAGAGTGCATAGTATCCCTGGGCACTGGACGTTATGAGAGT 2220
L W P D V P L E C I V S L G T G R Y E S
2221 GATGTGAGAAACACGCGTAACATACACAAGCTTGAAGAACTAAACTTTCTAATGTATCAAC 2280
D V R N T V T Y T S L K T K L S N V I N
2281 AGTGCTACAGATACAGAAGAAGTCCATATAATGCTTGATGGCCTGTTACCTCCTGACACC 2340
S A T D T E E V H I M L D G L L P P D T
2341 TATTTAGATTCAATCCTGTAATGTGAAACATACCTCTAGATGAAAGTCGAAATGAA 2400
Y F R F N P V M C E N I P L D E S R N E
2401 AAGCTGATCAGCTGCAGTTGGAAGGTTGAATACATAGAAAGAAATGACAAAAAATG 2460
K L D Q L Q L E G L K Y I E R N E Q K M
2461 AAAAAAGTTGCAAAAATATTAAGTCAAGAAAAAACAACCTCTGCAGAAAAATTAATGATTGG 2520
K K V A K I L S Q E K T T L Q K I N D W
2521 ATAAATTTAAAACTGATATGTATGAAGGACTTCCATTCTTTCAAAAATTTGTATGAGTA 2580
I K L K T D M Y E G L P F F S K L -
2581 TATGCTTATGTTCTCATTAATGAAGTCTGTTAGAAGATCAACCAATTCAATTAAGCAA 2640
2641 TTGTGGGTTGACATGAGTTAACTTTGAATACGTAATGATTTCTGAGAAATCCTGAAAA 2700
2701 AGACGGTCTTCAACCAAGCTTGCATAGCACAGAGAATAATCTTGTTACAGAAATTCATAT 2760
2761 GGAACTAGGCTTTTAAGATGTTAATAATTAAGCTTTAGTAACCTTACTGTGCTA 2820
2821 GTAGATTTTAGTAGATATGGTGTATATGTTGATGTTGAAAAATATATTAATATATG 2880
2881 TGCCGAACAAGAAACCGAAAGCTATATGTAATGTTTACTGTGATTTTACTTTAGTCCATAT 2940
2941 CATGTTGAATTTATGTGATCATTTGATTTTATTCATATGAAAAAGCTAATTTCTTCTTAA 3000
3001 ATTTACATTTACCTAATATTTCTACAGTATGTTCTCCCAATCCACACTGCCCTTTATTTGT 3060
3061 AATATCATCTAATAGATGACAGAAAAATGGAATTTCTCTATTAAGTATTTTACATTTG 3120
3121 ACATAAAAAAGAACAGATACAGTTTCTATTCAGATATGTTTATTTTAAACATTTGTTGG 3180
3180 TTAATAAAAGGTGAAGTCCAGTCAACCACTTTTACCCTGGAATTTCAAGATAATGCTA 3240
3241 TATTAACCTTTCCAGATCTAACACTAGCTTATTTCTCCCTGTTAATAAAATGTTGAACT 3300
3301 TACTGAGGAGATATCTCTATCATTTAACAAAAATTAATTTAATAATCTGTTGTTAA 3360
3361 AGGCTAATGTCAATTTTAAATTAATTTTGTTCATTAATGTAGCTCCCTTTAGCCTTTGA 3420

FIGURE 2

iPLA2 γ Splice Variants



open boxes are noncoding regions
shaded regions are putative coding regions
stippled lines represent intron splicing

Splice Variants of IPIA₂^γ
4/5/00

81 | Exon 2 | Exon 3 | 160

1 TGGGCGCTGCATCCCGATGTCTTCTCCTCCAGGTCTACATGATTACCTGAAGTTTATAAGTAGAGCCATGAATTATG

2 TGGGCGCTGCATCCG.....GTAGACCATGAATTATG

3 TGGGCGCTGCATCCCGATGTCTTCTCCTCCAGGTCTACATGATTACCTGAAGTTTATAA.....

C G L H P D C L L Q G L H D Y L K F N N

141
T V D I Y I Y L S N A R S V C G K Q R S K Q L Y F L 220
1 ACTGTAGATATATATATTACCTCCTTAGTAATGCAGAAGTGTGTGGGACGACAGAGAAGCAAGCAACTGTATTTCTT
2 ACTGTAGATATATATATTACCTCCTTAGTAATGCAGAAGTGTGTGGGACGACAGAGAAGCAAGCAACTGTATTTCTT
3TAATGCAGAAGTGTGTGTGGGACGACAGAGAAGCAAGCAACTGTATTTCTT
N A R S V C G K Q R S K Q L Y F L

FIGURE 4 (SHEET 1)

Full-length iPLA₂ γ

Primers for PCR amplification of full-length 88kDa iPLA₂ γ :

Sense primer M444 5'-TTTGTGACATGTCTATTATCTGACTGTAGATA-3'

Reverse primer M458 5'-GCATAGCATGCTCACAAATTTGAAAAGAATGGAAGTCC-3'

Sequence of 88kDa iPLA₂ gamma:

atgtctattaatctgactgtagatatatatattaccctccttagtaatgcaagaagtgtt
M S I N L T V D I Y I Y L L S N A R S V
tgtgggaagcagaagaagcaagaactgtatttctgttctcaccctaagcattactggagg
C G K Q R S K Q L Y F L F S P K H Y W R
ataagccacatcagtcctacaagaaggtttcatalacaacataataagatgttaaatggacc
I S H I S L Q R G F H T N I I R C K W T
aaaagtgaaagcacattcttgcaagtaagcaactgttactctccaagcaaccatggtttacat
K S E A H S C S K H C Y S P S N H G L H
attgggattttgaaacttagcactctctgtctcccaaggacttaccaaaagtgaaacatttgt
I G I L K L S T S A P K G L T K V N I C
atgtcccgatattaagaagtactttgaactctgtttccaaggctgttttggcaatccaat
M S R I K S T L N S V S K A V F G N Q N
gaaatgattccagtttagtccaatttaagccaagttcccaaatttaagaaaagttatcg
E M I S R L A Q F K P S S Q I L R K V S
gatagtgctgtttaaacagaaaacacatcaacaagccatcaaatctctgaaaaaatat
D S G W L K Q K N I K Q A I K S L K K Y
agtgcacaatcagcagaaaagtccttccagagaagaagaagtcacacattatagacaaa
S D K S A E K S P F P E E K S H I I D K
gaagaagatatagtaaacgcagctttttcattacacaagttctataaccacaaaattt
E E D I G K R S L F H Y T S S I T T K F
ggagactcatctactttttatcaaatcatattcaatattccaacgtaaggaaaaa
G D S F Y F L S N H I N S Y F K R K E K
atgtctcaacaaaaggaaaatgaacatttccgggacaatcagaacttgaagataaaaag
M S Q Q K E N E H F R D K S E L E D K K

FIGURE 4 (SHEET 2)

gtagaagaggggaaattaagatctccagatccctggcatccctggcttataagccaggctca
V E E G K L R S P D P G I L A Y K P G S
gaatctgtacatacgytggacaagcctacaagtccttctcgatatacctgatgttcttcaa
E S V H T V D K P T S P S A I P D V L Q
gttcaactaaacaagtalgtctaacttcttctcgtcccaaggaagtgtaacaagct
V S T K Q S I A N F L S R P T E G V Q A
ttaagtggtgtatatattgtgtgactgtccccaatlaaglatgatccaagaagtcag
L V G G Y I G G L V P K L K Y D S K S Q
tcagaagaacagggaagcctgtctaaactgatcaggctgtcagcaagacagaatgtca
S E E Q E E P A K T D Q A V S K D R N A
gaaggaagaaaaagcgttatctcttcagcgagaaaaagattatcgcaaggytgatgtat
E E K K R L S L Q R E K I I A R V S I D
aacaggaccgggcattagttcaggcattagaagaacaactgacccaagctctgcatt
N R T R A L V Q A L R R T T D P K L C I
actaggytgaagaactgacttctcattctctaagattcctgaaggaaaggyagtgct
T R V E E L T F H L L E F P E G K G V A
gtcaagggaagaattattccatatattattacgactgagacaatlaaggatgaactct
V K E R I I P Y L L R L R Q I K D E T L
caggctgcagttagagaatatttgccctaattggtatgtgatccagtgaaagggaga
Q A A V R E I L A L I G Y V D P V K G R
ggaatccgaattctctcaattgatgtgtgaggaacaaggcggtgtgtctctccagacc
G I R I L S I D G G T R G V V A L Q T
ctacgaaatlagttgaacttactcagaagccagtlcatcagctccttgattacattgt
L R K L V E L T Q K P V H Q L F D Y I C
ggtgtaagcacaggtgcatattagcttctcatgtgtgggtgttccatatgccccttgat
G V S T G A I L A F M L G L F H M P L D
gaaatgtgaggaacttatacgaaaaatlagatcagatgtatttccaaaaatgtccattgt
E C E E L Y R K L G S D V F S Q N V I V
ggaacagtaaaaatgagtgtaggccatgcatltaacacagtcacaacatggygaaaacatt
G T V K M S W S H A F Y D S Q T W E N I
cttaagtatagtgatgtcgtcactgatgtatgaacacagcaagaaccccacatgtcct
L K D R M G S A L M I E T A R N P T C P
aaggtagctgtgtaagtaaccatagtaaatagaggataacaccaagaagcttctgtctc

FIGURE 4 (SHEET 3)

K V A A V S T I V N R G I T P K A F V F
 agaactatgtcatttttccttgaatcaactcatttatttggaggctgtcagtaaa
 R N Y G H F P G I N S H Y L G G C Q Y K
 atgtgcaggccattagagcctcatctgtgtctccaggctacttgcagaatatgcaty
 M W Q A I R A S S A A P 'G Y F A E Y A L
 ggaatgatcttcatacagaatggaggttcttctgaataacccttcggcattagctatg
 G N D L H Q D G G L L N N P S A L A M
 catgagtgtaaatgtcttggccagatgtgccgttagagtgcatagtatccctgggcaat
 H E C K C L W P D V P L E C I V S L G T
 ggacgltatgagagtgatgtgagaaacacggttaacatacacaagcttgaaaaactaaactt
 G R Y E S D V R N T V T Y T S L K T K L
 tctaattgtatacaacagtgctacagatacagaagaagtcacataataatgttgatggcctg
 S N V I N S A T D T E E V H I M L D G L
 ttacctcctgacacccatttttagatlcattccctgtlaatgttgtaaaacatacccttagat
 L P P D T Y F R F N P V M C E N I P L D
 gaaagtcgaaatgaaaagcttgatcagctgcagttggaagggttgaatacatagaaaga
 E S R N E K L D Q L Q L E G L K Y I E R
 aatgaacaaaaaatgaaaaagltgcaaaaatatlaagtcagaagaaaaaacactctgcag
 N E Q K M K K V A K I L S Q E K T T L Q
 aaatlaatgattgataaaatlaaaactgatatgtatgaaggacttccattcttltca
 K I N D W I K L K T D M Y E G L P F F S
 aaattgtga
 K L -

FIGURE 5 (SHEET 1)

Sequence of 77kDa iPLA2 gamma:
starting at amino acid 101 (nucleotide 301)

Primers for PCR amplification of 77kDa iPLA2γ:

Sense primer m534

5'-TGAACGTCGACATGTCCCGTATTAAAA-3'

Reverse primer M458

5'-GCATAGCATGCTCACAATTGTGAAAAGAATGGAAGTCC-3'

atgtcccgatatataaagtactttgaactctgtttccaagctgtttttgccaatcaaat
M S R I K S T L N S V S K A V F G N Q N
gaatgatttcacglttagctcaatttaagccaagttcccaattttaagaaaagtatcg
E M I S R L A Q F K P S S Q I L R K V S
gatatggctgtttaaacacagaaaaacatcaaacaggccatcaatctctgaaaaatat
D S G W L K Q K N I K Q A I K S L K K Y
agtgaacaatcagcagagaaaaagatcctttccagaagagaaaaagtcacattatagacaaa
S D K S A E K S P F P E E K S H I I D K
gaagaagatatagtaaacgcagctcttttcatcacacaagttctataaccacaaaattt
E E D I G K R S L F H Y T S S I T T K F
ggagactcattctactttttatccaatcatatatattcaaacgtaaggaaaaa
G D S F Y F L S N H I N S Y F K R K E K
atgtctcaacaagaagaatgaacatttccgggacaatcagaacttgaagataaaaag
M S Q Q K E N E H F R D K S E L E D K K
gtagaagagggaatlaagatctccagatccttgcatcctgtgtataagccaggctca
V E E G K L R S P D P G I L A Y K P G S
gaatctgtacatacgttgacaagcctacaagtccttctgcgatacctgatgttcttcaa
E S V H T V D K P T S P S A I P D V L Q
gttccaactaaacaagtatgtctaactttcttctcgtgccacggaagtggtacaagct
V S T K Q S I A N F L S R P T E G V Q A
ttagtagtggtatattgtgtgactgtccccaattaaagratgatccaagagtcag
L V G G Y I G G L V P K L K Y D S K S Q
tcagaagaacaggaagagcctgtctaaaactgatcaggctgtcagcaagacagaatgca
S E E Q E E P A K T D Q A V S K D R N A

gagagagaaaaagcgtttatctctcttcagcggagaaaaagattatcgcgaaggtgtgagtattgat
E E K K R R L S L Q R E K I I A R V S I D
aacagagaccgggcattagttcagycattaaagaagaacaactgaccccaagctctgcatt
N R T R A L V Q A L R R T T D P K L C I
actagggltgaagaactgacttcttcacctctctagaatttcctcgaagaaagagagtgct
T R V E E L T F H L L E F P E G K G V A
gtcaaggaaagaattatccacataattattacgactgagacaattaaggtgaactctt
V K E R I I P Y L L R L R Q I K D E T L
caggtctgagttagagaattttggccctaattggtctatgtgtgattccagtgaaaggagag
Q A A V R E I L A L I G Y V D P V K G R
ggaatccgaattctctcaattgtatgtggaggaacaaggcgctgtgtctctccagacc
G I R I L S I D G G G T R G V V A L Q T
ctcagaaaattagttgaacttactcagaagccagttcatcagctctttgattacattgt
L R K L V E L T Q K P V H Q L F D Y I C
ggtgtgaagcacaggtgcccattatgacttctcatgttggtgtgtttccatatcccttgat
G V S T G A I L A F M L G L F H M P L D
gaatgtgaggaactttatcgaaaaattagagatcagatgttatttccacaaaatgtcatgtt
E C E E L Y R K L G S D V F S Q N V I V
ggaacagtaaaaaatgagttggagccatgcatlittatgacagtcacaaacatgvgaaaaacatt
G T V K M S W S H A F Y D S Q T W E N I
cttaaggatagagatggtatctgcactgtatgtatgtaaacagcaagaaaccccatgtcct
L K D R M G S A L M I E T A R N P T C P
aaggtagctgtgtgaagtacatagtaaatagagggatbaacaccacaaagcttltgttctc
K V A A V S T I V N R G I T P K A F V F
agaactatgttcatttctcctggaatcaactctcatlatttgggaggtgtcagtataaa
R N Y G H F P G I N S H Y L G G C Q Y K
atgtgacagccatttagagcctcatcctgtctccaggtcacttgcagatatatgcattg
M W Q A I R A S S A A P G Y F A E Y A L
ggaatgatcttcacatcaagatgaggttctctcgaataaaccttcggcatthagctatg
G N D L H Q D G G L L L N N P S A L A M
catgagtgtaaatgtctcttggccagatgtgcgcgttagagtgcatagttatccctgggcact
H E C K C L W P D V P L E C I V S L G T
ggacgcttatgagagtgatgttgagaacacacggttaacatcacacaagcttgaaaactaacctt

FIGURE 5 (SHEET 3)

FIGURE 6 (SHEET 1)

Sequence of 74kDa iPLA2 gamma:
starting at amino acid 122 (nucleotide 364)

Primers for PCR amplification of 74kDa iPLA2 γ :

Sense primer m533 5'-TCAAGTCGACATGATTTCACGTTAGC-3'
Reverse primer M458 5'-GCATAGCATGCTCACAAATTTGAAAGAATGGAAGTCC-3'

atgatttcacgcttagctcaatttaagccaagttcccaattttaagaaaagtatcg
M I S R L A Q F K P S S Q I L R K V S
gatatgctggtttaaaccagaaaaacatcaacaagccatcaatctctgaaaaatat
D S G W L K Q K N I K Q A I K S L K K Y
agtgcacaatcagcagaaaaagagtcctttccagaaagagaaaagtcacattatagacaaa
S D K S A E K S P F P E E K S H I I D K
gaagaagatatagtaaacgcagctcttttccattacacaaagttctataaccacaaaattt
E E D I G K R S L F H Y T S S I T T K F
ggagactcattctacttttlatcaaatcatalttaattcatattccaacgtaaggaaaaa
G D S F Y F L S N H I N S Y F K R K E K
atgtctcaacaagaagaatgaacattccgggacaatcagaacttgaagataaaaag
M S Q Q K E N E H F R D K S E L E D K K
gtagaagagggaatataagatctccagatccctgcatccctgcttataagccaggtca
V E E G K L R S P D P G I L A Y K P G S
gaatctgtacatacgttgacaagcctacaagtccttctgcgatacctgatgttcttcaa
E S V H T V D K P T S P S A I P D V L Q
gtttcaactaacaagtatgtctaactttcttctcgtccacggaagtgtaacaagct
V S T K Q S I A N F L S R P T E G V Q A
ttagtagtggttatattgtgtgactgtlccccaatttaagtatgatccaagagtcag
L V G G Y I G G L V P K L K Y D S K S Q
tcagaagaacaggaagagcctgtctaaactgatcaggctgtcagcaagacagaatgca
S E E Q E E P A K T D Q A V S K D R N A
gaggaagaaaaagcgtttatctcttcagcgagaaaaagattatcgcaagggtgagtattgat
E E K K R L S L Q R E K I I A R V S I D

FIGURE 6 (SHEET 2)

aacaggaccgggcattagttcaggcattaaagaacaactgacccaagctctgcatt
N R T R A L V Q A L R R T T D P K L C I
actagggttgaagaactgacttttcattctctagaatttcctgaagaaaggagtggt
T R V E E L T F H L L E F P E G K G V A
gtcaagaaagaattatccatatttattacgactgagacaattaagatgaactcct
V K E R I I P Y L L R L R Q I K D E T L
caggctgcagttagagaattttggccctaattggtatgtggtaccagtgaaggaga
Q A A V R E I L A L I G Y V D P V K G R
ggaatccgaattctcattgatgtgtggaagaaaggggcggtgtctctccagacc
G I R I L S I D G G T R G V V A L Q T
ctacgaaaattagttgaacttactcagaagccagttcactcgtcttgattacattgt
L R K L V E L T Q K P V H Q L F D Y I C
ggtgtaagcacagtgccatatagcttcatgttggtgtttcatatgcccctggat
G V S T G A I L A F M L G L F H M P L D
gattgtgaggaacttatacgaaaattagatcagatglatlccacaaatgtcatgtt
E C E E L Y R K L G S D V F S Q N V I V
ggaacagtaaaaatgagttggagccatgcatlctatgacagtcacaacatgggaaacatt
G T V K M S W S H A F Y D S Q T W E N I
cttaagatatgagtggtctgcactgatgttgaaacagcaagaacccccacatgctc
L K D R M G S A L M I E T A R N P T C P
aagtagctgtgtagtaagcatagtaaatagagggataacacccaagcttltgttc
K V A A V S T I V N R G I T P K A F V F
agaactatgtcatlcttcctggaatcaactctcatlcttgggaggtgtcagtataa
R N Y G H F P G I N S H Y L G G C Q Y K
atgtggcagggcattagagccctcatctgtctgccaggtacttgcagaatatgcaty
M W Q A I R A S S A A P G Y F A E Y A L
ggaatgatcttcatcaagatgaggttcttctgaataacccttcgcatltagctatg
G N D L H Q D G G L L L N N P S A L A M
catgagtgtaatgtcttctggccagatgtgcccgttagagtgcataglatccctgggcact
H E C K C L W P D V P L E C I V S L G T
ggacgttatgagagtgatgtgagaacaacggttaacatacaagaagcttgaaactaaact
G R Y E S D V R N T V T Y T S L K T K L
tctaattgttatacaacagtgctacagatatacagaagaagttccatataatgttgatggcctg

S N V I N S A T D T E E V H I M L D G L
 ttacctctgcacacctattttagattcactcctgtgaatgtgtgaaaaacacatcctctagat
 L P P D T Y F R F N P V M C E N I P L D
 gaaagtcgaaatgtaaaagctgcatcagctgcagttggaagggttgaatatacatagaaga
 E S R N E K L D Q L Q L E G L K Y I E R
 aatgaacaaaaaatgtaaaaaagttgcataaaatatgaagtcagaataaaacaactctgcag
 N E Q K M K K V A K I L S Q E K T T L Q
 aaaaattaatgatgtgataaaatlaaaaactgatatgtatgaaggacttccattctttca
 K I N D W I K L K T D M Y E G L P F F S
 aaattgtga
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FIGURE 7 (SHEET 1)

Sequence of 63kDa iPLA2 gamma
starting at amino acid 221 (nucleotide 661)

Sense primer M530

5'-GTAAGTCGACATGTCTCAACAAAGG-3'

Reverse primer M458

5'GCATAGCATGCTCACAATTGAAAGAATGGAAGTCC-3')

atgtctcaacaaaggaaatgaacattccgggacaatcagaacttgaagataaaaag
M S Q Q K E N E H F R D K S E L E D K K
gtagaaggagggaattaatgaatctccagatccctggcatccctgtgtataaaggcaggtca
V E E G K L R S P D P G I L A Y K P G S
gaatctgtacatacgttgacaagcctacaagtccttctcgataccctgatgttctcaa
E S V H T V D K P T S P S A I P D V L Q
gtttcaactaacaagaatgtatgttaacttcttctctgtccacggaagtgylacaagct
V S T K Q S I A N F L S R P T E G V Q A
ttagtagtggtatatgtgttgactgtgtcccaatlaaagtatgatccaagagtcag
L V G G Y I G G L V P K L K Y D S K S Q
tcagaagaacaggaagagcctgtctaaactgatcaggtgtcagcaagaagacagaatgca
S E E Q E E P A K T D Q A V S K D R N A
gaagagaanaaagcgtttatctcttcagcgagaagaagattatcgcaagggtgagtatgat
E E K K R L S L Q R E K I I A R V S I D
aacagagcccggtcattagttcagcgatlaagaagaacactgacccaagctctgcatt
N R T R A L V Q A L R R T T D P K L C I
actaggttgaagaactgacttcttcatcttcttagaatctcctgaaggaaaggagtggt
T R V E E L T F H L L E F P E G K G V A
gtcaaggaaagaattatcccatatttatcagactgagacaatlaaggatgaactctt
V K E R I I P Y L L R L R Q I K D E T L
caggtcgagttagagaatatttgccctaatgtgctatgtggtccagtgaaagggaga
Q A A V R E I L A L I G Y V D P V K G R
ggaatccgaattctcgaattgatgtgtgaggaacaagggtgtgtgtctccagacc
G I R I L S I D G G T R G V V A L Q T
ctacgaaaattagttgaacttactcagaagccagttcatcagctcttattacatttgt
L R K L V E L T Q K P V H Q L F D Y I C

ggtgtgaagcaccaggtgtgccatattagcttccatgttgggtgttccatattgccccttgat
 G V S T G A I L A F M L G L F H M P L D
 gaatgtgaggaactttatcogaaaattagatcagatgtratttccacaaatgtcatgtt
 E C E E L Y R K L G S D V F S Q N V I V
 ggaaccagtaaaaatgagttggagccatgtcatttattagcacagtcacaacatggaacaactt
 G T V K M S W S H A F Y D S Q T W E N I
 cttagagtagagatggatctgtcactgtatgttgaacacgcaagaacccccacatgtcc
 L K D R M G S A L M I E T A R N P T C P
 aaggtagctgtgttaagtagccatagtaaatagaggatbaacacccaaagcttltgttc
 K V A A V S T I V N R G I T P K A F V F
 agaacattatgtcatcttccctggaatcacctcattatttgggaggtgtcagtataaa
 R N Y G H F P G I N S H Y L G G C Q Y K
 atgtggcagggccattagagccctcatctgtctgtccaggctacttgcagatatgtcatgt
 M W Q A I R A S S A A P G Y F A E Y A L
 ggaatatgatcttcatacagaatggagtttgccttcttgataaaccttcggcattagctatg
 G N D L H Q D D G G L L L N N P S A L A M
 catgagtgtaaaatgtcttggccagatgtgcggttagagtgcatagtatccctgggcact
 H E C K C L W P D V P L E C I V S L G T
 ggcagcttatgagagtgatgtlgagaacacgcgtlaacatcacacaagcttgaanaactaaactt
 G R Y E S D V R N T V T Y T S L K T K L
 tctaatgttatccaacagtgctacagatacagaagaagtcacatatatgtcttgatggcctg
 S N V I N S A T D T E E V H I M L D G L
 ttacctctgcacacctattttagattcaatccctgtaatgtgtgaaaaacatatccttagat
 L P P D T Y F R F N P V M C E N I P L D
 gaaagtcgaatatgaaaagctgtgatacagctgcagttggaaaggttgaatatacatagaaga
 E S R N E K L D Q L Q L E G L K Y I E R
 aatgaacaaaaaatgaaaaaagtgtcaaaaaatattaaagtcagaagaaaaaacacactctgcag
 N E Q K M K K V A K I L S Q E K T T L Q
 aaaaattaatgatgtgataaaattaaaaactgatatgttatgaaggacttccattctttcca
 K I N D W I K L K T D M Y E G L P F F S
 aaattgtga
 K L -

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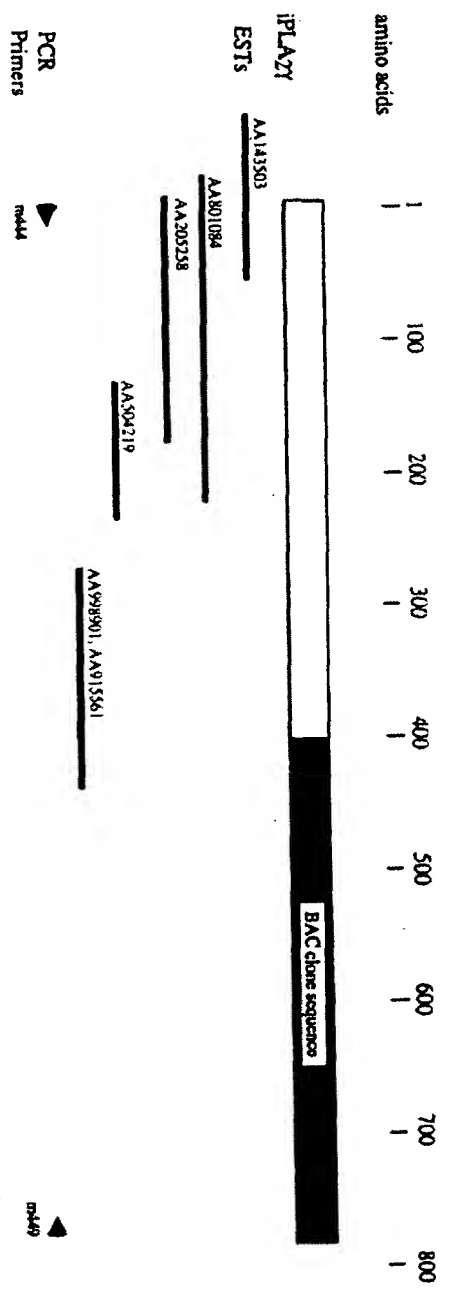


Fig. 8

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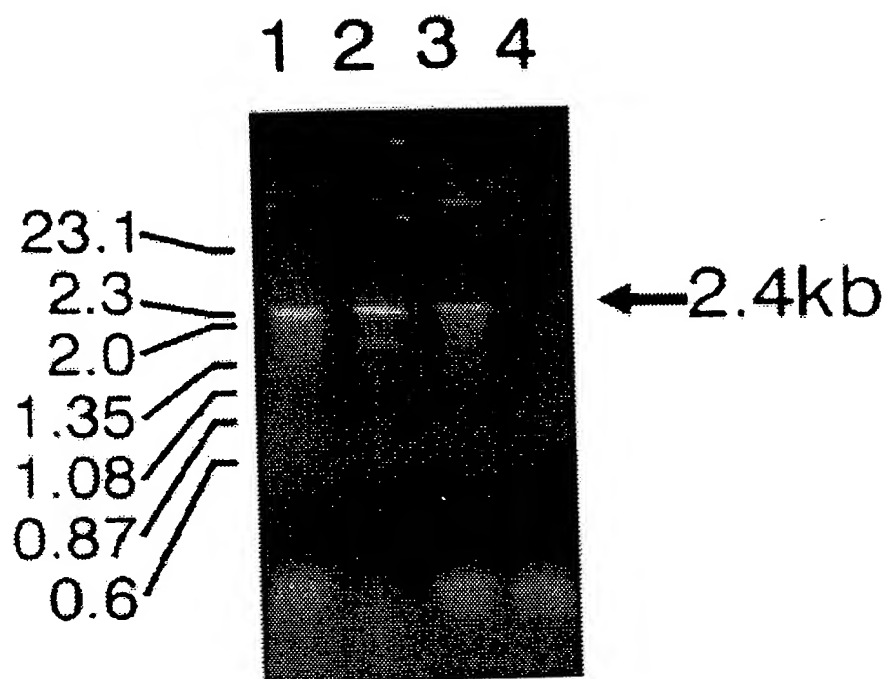
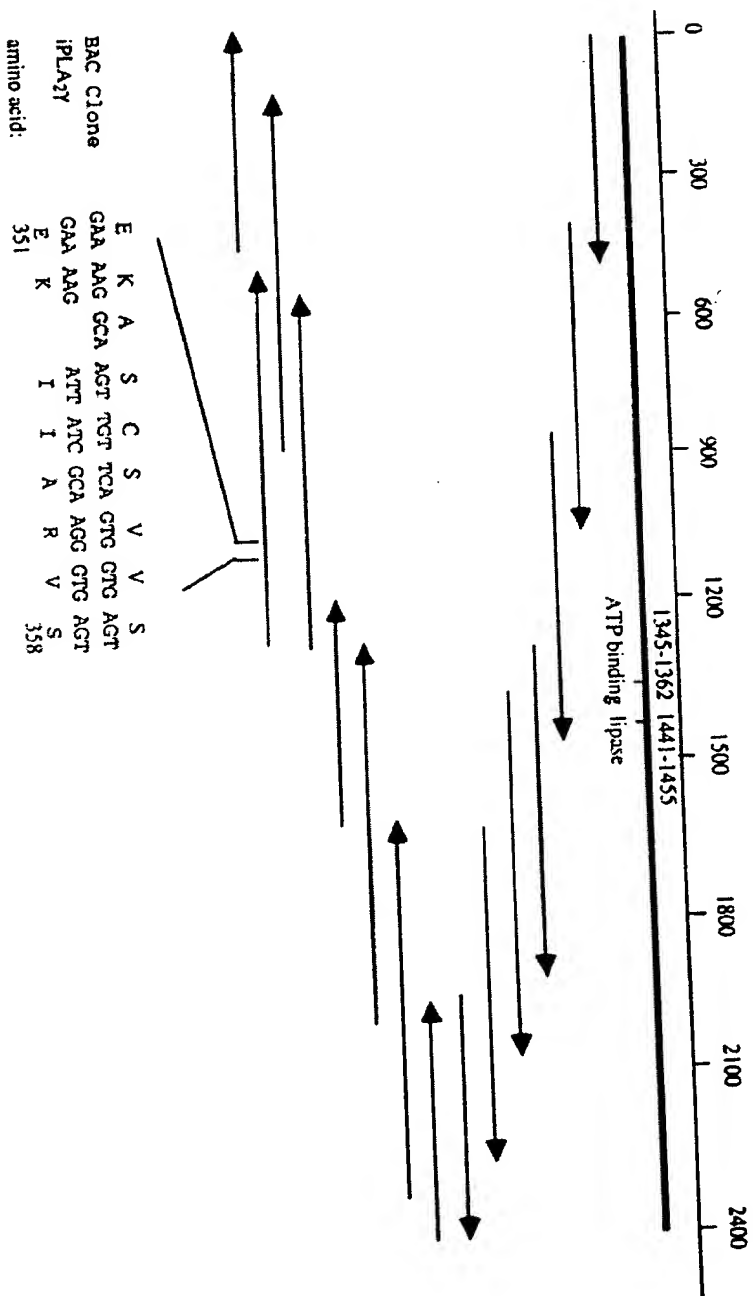


FIG. 9



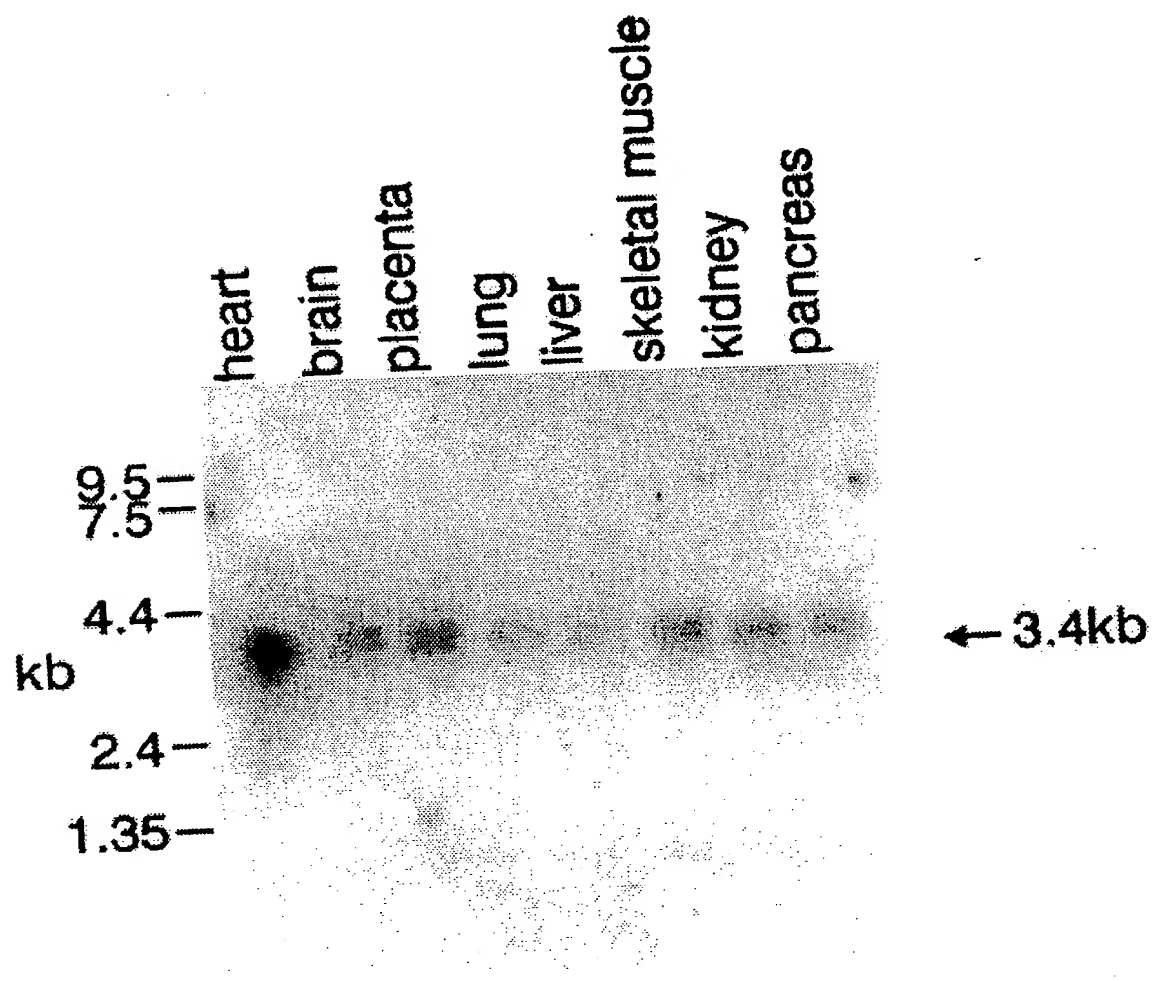


FIG. 12



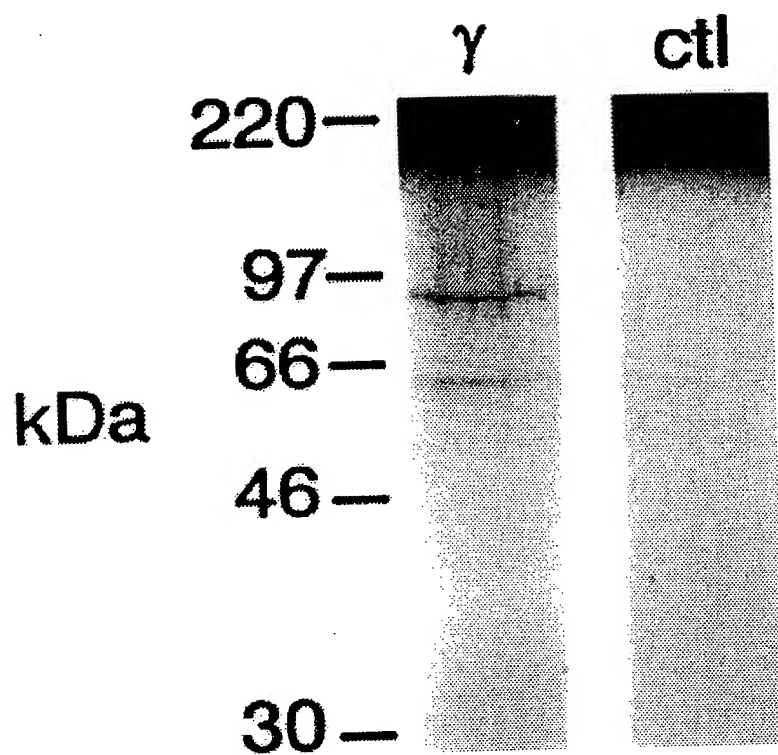


FIG. 14

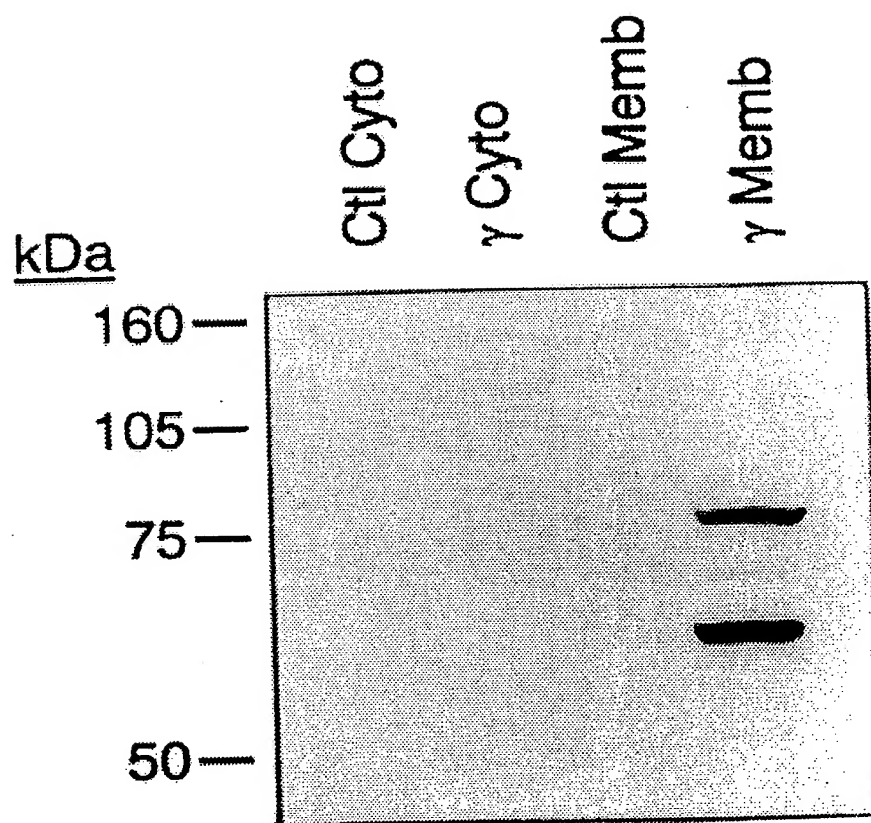


FIG. 15

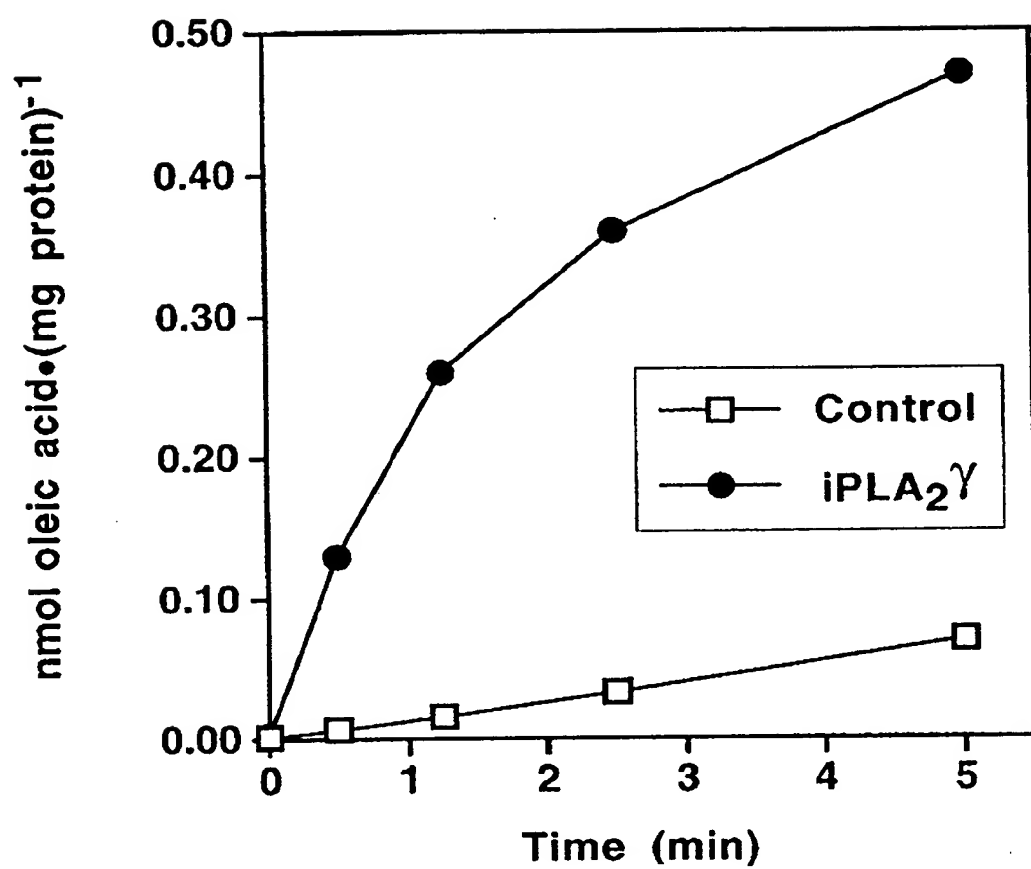


FIG. 16

FIG. 17

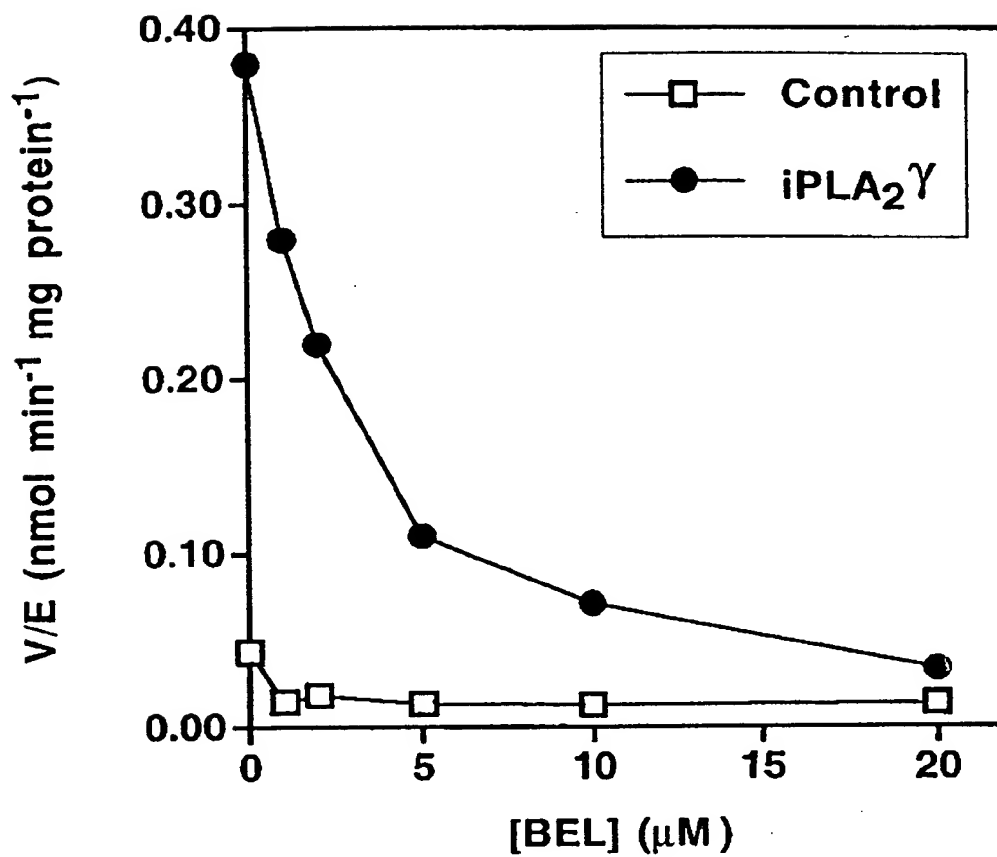


FIG. 18

Translational Repression of iPLA₂γ

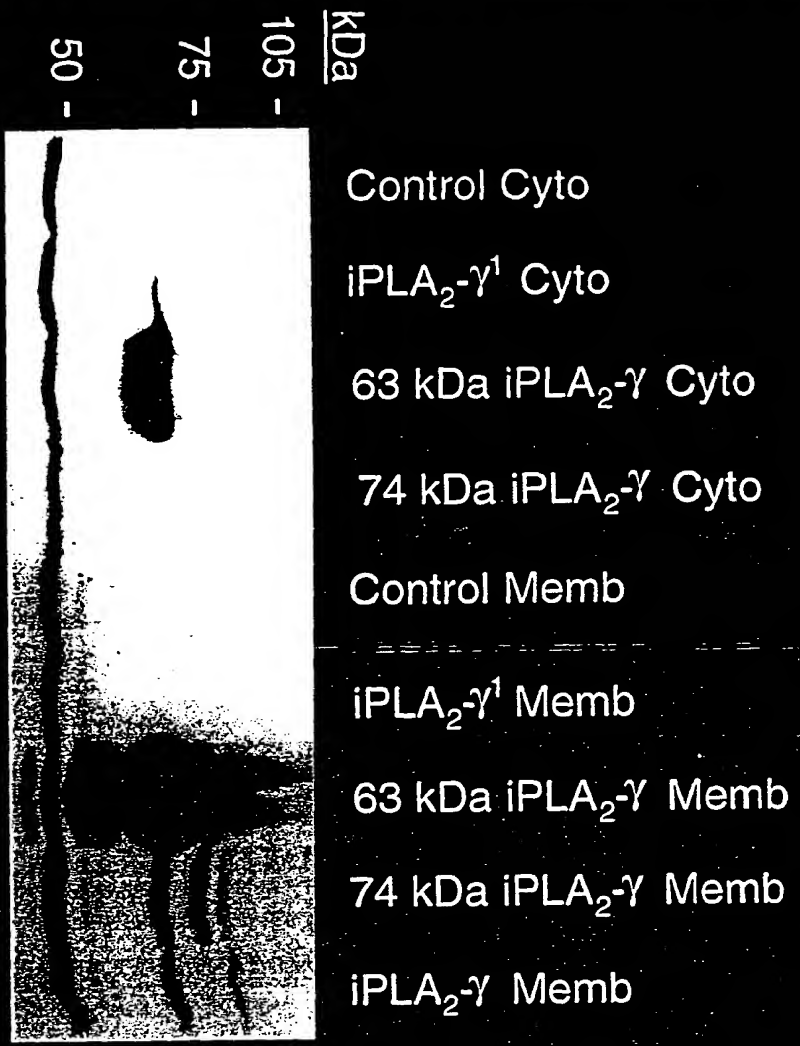


FIG. 19

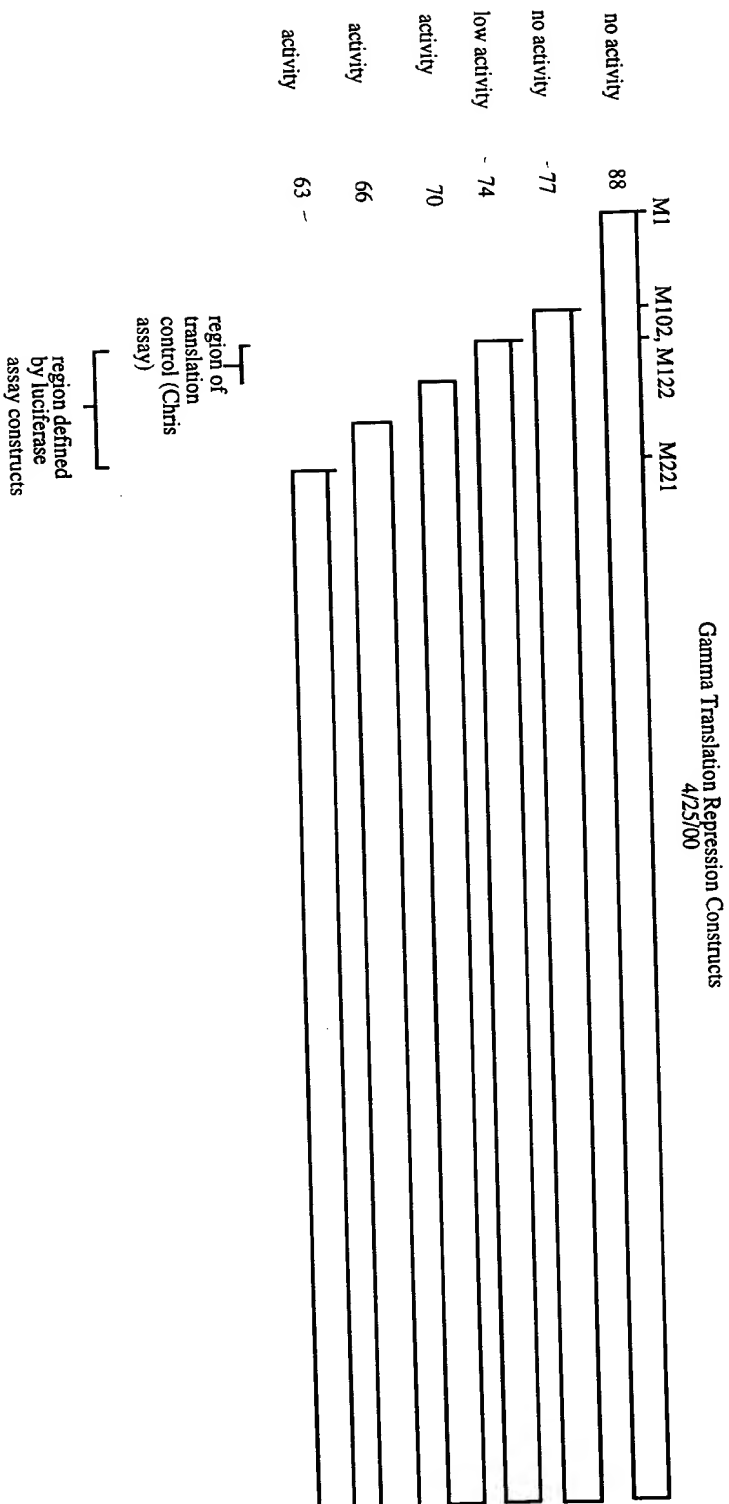


FIG. 20

FIG. 20 is a horizontal bar chart showing the activity of various Gamma Translation Repression Constructs. The y-axis lists the constructs: M1, M102, M122, and M221. The x-axis represents activity levels, with values 88, 77, 74, 70, 66, and 63. The activity levels are categorized as 'no activity' for M1 and M102, 'low activity' for M122, and 'activity' for M221 and the two unlabeled constructs. A bracket indicates that the region of translation control (Chris assay) is defined by the constructs M102, M122, and M221. Another bracket indicates that the region defined by luciferase assay constructs is defined by the constructs M122, M221, and the two unlabeled constructs.

Additionally, iPLA2y sequences were inserted by ligation of 15-23mer annealed phosphorylated oligonucleotide pairs 5' of full-length luciferase coding sequence cloned into pFASTBAC via NotI/XbaI restriction sites and then luciferase activity of recombinant protein produced in the Sf9 system was subsequently measured using the Luciferase Assay System of Promega.

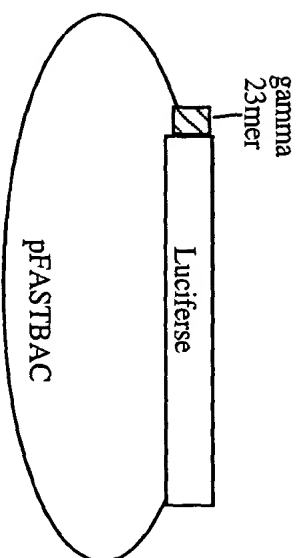


FIG. 21

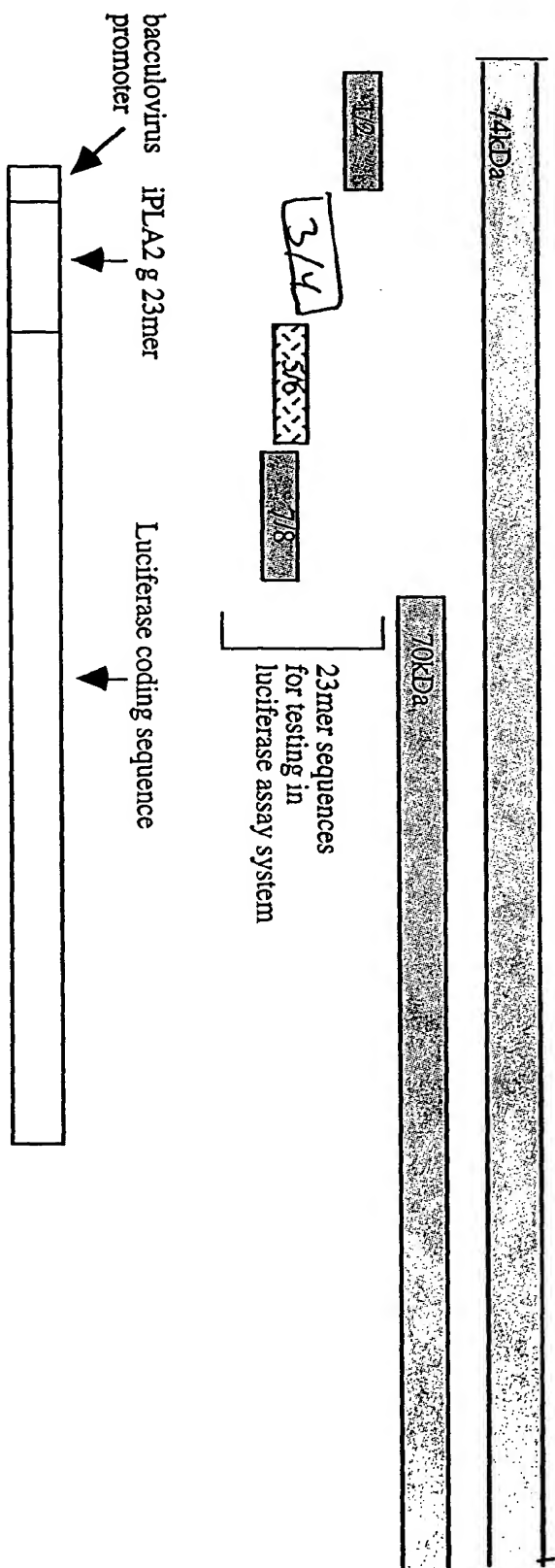


FIG. 22

Phosphorylated oligo pairs for sequence between nucleotide 364- 455
for translational repression
of iPLA2 gamma in the luciferase expression system:

iPLA2γ	atgattcacggttagctcaatttaagccaagttcccaattttaagaagatcggatagtggtgttaaaacagaaaacatcaaca
1/2	tcgacctgatttcacggttagtcaatt ggactaaagtgcgaatcgagttaacg
3/4	tcgactaagccaagttcccaatttaa gattcgggttcaagggtttaaatccg
5/6	tcgacgaaaagtatcgatagtgctgg gctttcatagcctatcacgaccccg
7/8	tcgacttaaaacagaaaacatcaaca gaatttgccttttctgtagttgtccg

FIG. 23

Phosphorylated oligo pairs for sequence between nucleotide 364- 455
for translational repression
of iPLA2 gamma in the luciferase expression system:

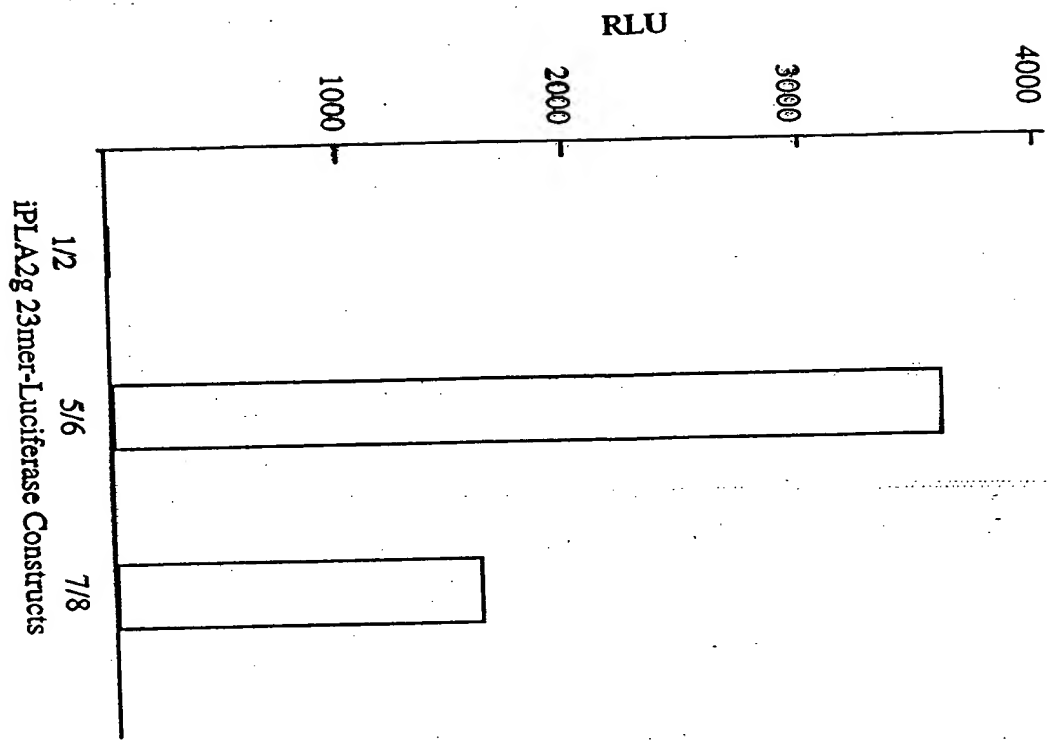


FIG. 24

FIG. 24 is a bar graph showing the relative luciferase activity (RLU) for three different iPLA2g 23mer-Luciferase Constructs. The y-axis is labeled 'RLU' and ranges from 0 to 4000. The x-axis is labeled 'iPLA2g 23mer-Luciferase Constructs' and has three categories: 1/2, 5/6, and 7/8. The bars are white with black outlines. The 1/2 construct shows the highest activity, followed by the 5/6 construct, and then the 7/8 construct.